

Hybrid machine learning model towards neuroimaging analysis for detection and grading brain tumors

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ABSTRACT

Neuroimaging analysis enables detailed observation of brain tumors, with growing adoption of advanced imaging techniques in clinical practice. Limitations of conventional approaches in supporting proactive decision-making and reliable grading are increasingly addressed through machine learning. However, earlier models often faced challenges of limited generalization and computational burden. To overcome these issues, this study introduces a hybrid convolution neural network–support vector machine (CNN–SVM) framework that combines ResNet-50 feature extraction with a feature weighting (FW) strategy and SVM-based classification for improved diagnostic precision. The system is further enhanced with a clinically guided grading scheme, mapping classification outputs into malignant, benign, and healthy categories for greater interpretability. The proposed model was evaluated on three benchmark neuroimaging datasets (Figshare, Kaggle magnetic resonance imaging (MRI), and BraTS-2019) and achieved up to 98.6% accuracy with high sensitivity and specificity, while retaining low computational cost and rapid inference, outperforming conventional CNN-only methods.

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1. INTRODUCTION

The term neuroimaging defines about utilization of different forms of an imaging approaches for visually investigating characteristics, size, location, and structure of tumor residing in brain [1]. The role of neuroimaging is significantly bigger as it contributes to monitoring the state of brain tumor followed by facilitating diagnosis and treatment planning. In current era, neuroimaging is carried out using positron emission tomography (PET), computed tomography (CT), and magnetic resonance imaging (MRI) [2]. There are also certain advanced and sophisticated form of neuroimaging (e.g., MR spectroscopy, diffusion tensor imaging (DTI), and functional MRI (fMRI)). Apart from detecting the presence of brain tumor, neuroimaging also assists in determining the state of benign or malignancy which guides oncologist and neurosurgeon for choosing their most effective treatment or procedure plans. However, there are also certain critical challenges in analysis of neuroimaging. The primary challenge is to differentiate different forms of tumor tissue, healthy brain tissue, and surrounding edema just from neuroimages using conventional imaging approaches [3]. The

frequently adopted CT and MRI have the higher chances to bypass detection of either very small tumors or tumors in early stages. They also cannot be used to determine the tumor recurrence or certain changes which could be due to treatment (radiation necrosis) [4]. Apart from this, it is also noted that the interpretation of neuroimaging is highly subjective (i.e., it completely depends upon expertism of radiologist and no automated system is ever in practical exercised). Existing diagnostic practices in healthcare units doesn't have any provision for multimodal data integration which calls for carrying out analysis on combined data from multiple imaging techniques for more granular investigation of severity of brain tumor. Existing studies shows that such issues have greater possibility to be addressed using machine learning methods [5], [6]. By inducing automation of image analysis, machine learning models can minimize subjectivity and increase accuracy. It is feasible for machine learning models to learn from large dataset, identify some explicit patterns, and use them for precisely detection and classifying tumor-related tissue from healthy one. However, irrespective of an immense potential and capability of complex state of analysis, machine learning methods still encounters some serious shortcomings too. The primary one is its higher dependencies towards well-labeled and larger size of dataset, which is not always possible to obtain from real-environment. Overfitting and data imbalance is another problem associated with existing dataset reducing the reliability of existing approaches. Hence, there is a need to evolve up to more innovative, simplistic, and yet robust approach which looks into the practical side of its application deployment and necessarily create a design accordingly.

The related work has been studied to understand frequently used machine learning methods for detection and classification of brain tumor. Support vector machine (SVM) is one of the frequently adopted machine learning methods meant for segregating tumor from non-tumor region [7]–[9]. Existing studies has shown increased accuracy but certain degradation is noted in presence of overlapping and noisy data. Detection of brain tumor is also carried out by random forest (RF) [10]–[12] and decision tree (DT) [13], [14]. In case of RF-based methods, multiple DTs are combined to study and enhance accuracy to find reduced overfitting and ability to handle-high dimensional data; however, it encounters maximized computational complexity when subject to many trees. On the other hand, DT approaches are quite simplified and often seen to be implemented as ensemble learning methods offering faster computation. However, DT usually cast low accuracy scores and has a tendency to overfit. In perspective of deep learning (DL), convolution neural network (CNN) is witnessed to offer impressive accuracy performance with autonomous feature extraction for brain tumor detection and classification. Existing studies in CNN [15]–[17] have proven its efficiency with complex image data; however, they have dependencies of massive labeled dataset with increased computational power. CNN cannot perform processing of sequential data and hence it is often found integrated with long short-term memory (LSTM) [18]–[20]. However, LSTM doesn't perform well when subjected to purely spatial image data. There is another variant of DL approach known as autoencoder that learns compressed representation of brain image for detect the anomalies [21], [22]. Although autoencoders offers effective dimensionality reduction and unsupervised feature learning, but they suffer from loss of information during compression.

The research problem identified after reviewing the existing literatures are as follows: i) there is a lack of generalization over different types of dataset observed training the existing models on specific dataset or limited dataset, ii) there are insufficient and innovative research methods for multi-class classification as majority of approaches emphasizes on binary classification while they struggle to offer optimal accuracy performance for multiple sub-types of brain tumor, and iii) there is no specific claim of existing approach towards balancing computational burden with accuracy; further, no simplicity in cases of modular approach being noted which could have offers ease in computational process. All these identified research problems have been addressed in proposed scheme where hybridization of machine learning models have been utilized.

The aim of the proposed study is to design a smart and efficient neuroimaging analysis by harnessing the hybridization of machine learning models towards facilitating precise grading of brain tumors obtained from radiological imageries. The novel contribution made by the proposed study are as follows: i) the study presents a hybrid CNN–SVM architecture that employs ResNet-50 for spatial feature extraction with an integrated feature weighting (FW) strategy, followed by SVM-based classification for improved decision boundaries, ii) the model is evaluated on three benchmark datasets to demonstrate its robustness and consistency under multi-class and binary settings, iii) the hybrid framework ensures a modular pipeline where feature extraction and classification are decoupled, allowing independent tuning and efficient adaptation across datasets, and iv) a clinically guided grading scheme is introduced to map classification outputs into diagnostically relevant categories (malignant, benign, and healthy), thereby enhancing interpretability and practical relevance. Additionally, comparative and ablation studies are conducted to validate that the adopted methodology in the proposed CNN–SVM system.

2. METHOD

The prime objective of the proposed study is to design a hybrid neuroimaging framework capable of classifying and clinically grading brain tumors with high reliability. The adopted methodology, shown in Figure 1, integrates deep feature extraction using a pre-trained CNN with robust classification through an SVM. The framework is carefully structured to ensure reliable tumor detection across multiple datasets while maintaining clinical interpretability. The first module of the proposed system is the data acquisition, where benchmark MRI datasets are employed for evaluation. To enhance data quality, a preprocessing operations are applied, which includes skull-stripping to remove non-brain tissues, image cropping to focus on the brain region, and resizing with normalization for consistent model input. The adopted preprocessing step ensures retaining of the region of interest along with eliminating irrelevant information.

The preprocessed images are then subjected to ResNet-50 CNN with transfer learning to extract features, where the convolutional layers capture hierarchical spatial representations. A global average pooling (GAP) layer is applied, followed by a FW mechanism that emphasizes more discriminative feature channels, ensuring better representation of subtle tumor-specific patterns. The resulting feature maps are flattened to construct a compact feature vector. These extracted features are then fed into a multi-class SVM classifier configured with probability estimation, which performs the final classification into four diagnostic categories: glioma, meningioma, pituitary tumor, and no tumor. Finally, the trained model is evaluated with multiple datasets, where performance is measured in terms of accuracy, precision, recall, specificity, sensitivity, and F1-score.

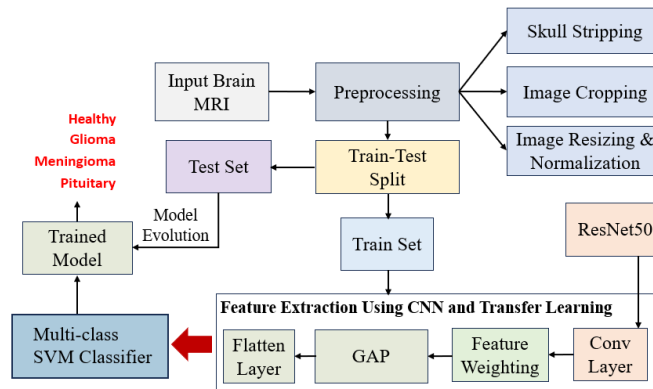


Figure 1. Adopted architecture of proposed hybrid model

2.1. Dataset description and experimental setup

This section describes the datasets and the experimental setup adopted for evaluating the proposed hybrid CNN–SVM framework. Three publicly available benchmark datasets of brain MRI images are used to ensure robust analysis under different classification settings. The first dataset is obtained from Figshare and contains 3064 T1-weighted contrast-enhanced MRI slices collected from 233 patients. Table 1 presents the overall dataset distribution and the associated classification tasks.

Table 1. Shows details of dataset distribution

Dataset	Classification tasks	Training samples	Testing samples	Total
Figshare [23]	Glioma, meningioma, and pituitary	2757	307	3064
BraTS 2019 [24]	Tumor and no tumor	2800	200	3000
Kaggle MRI [25]	Glioma, meningioma, pituitary, and no tumor	5712	1311	7023

The images are divided into three tumor types: glioma (1426 slices), meningioma (708 slices), and pituitary tumor (930 slices). For this study, the dataset is reorganized into a training set of 2604 samples and a testing set of 460 samples. This dataset is used for a three-class classification task. The second dataset is sourced from Kaggle and includes 7023 MRI images categorized into four classes: glioma, meningioma, pituitary tumor, and no tumor. From this dataset, 5712 samples are used for training and 1311 samples are used for testing. This dataset allows evaluation of the framework on a four-class classification task that includes both tumor cases and healthy scans. The third dataset is BraTS 2019, also obtained from Kaggle,

which is designed for binary classification. It consists of 2800 training samples and 200 testing samples divided into two classes: tumor and no tumor. This dataset helps to analyze the framework performance in detecting the presence or absence of tumors.

2.2. Data preprocessing

In order to ensure consistency and improve the quality of neuroimaging data prior to feature extraction, a comprehensive preprocessing operation is applied over input images. The preprocessing steps were designed to work on all three datasets to remove irrelevant information, and enhance brain tissue visibility, and prepare the images in a format suitable for the CNN–SVM model. The implementation process of the preprocessing operation is discussed in the Algorithm 1.

The first operation is carried out towards stripping the non-brain tissues such as skull, scalp, and surrounding structures using intensity-based thresholding, morphological filtering, and largest connected component analysis. Afterwards, the brain mask was localized by identifying its bounding box through contour detection, where each image is then cropped tightly around the brain region to eliminate empty background areas. These operation basically ensures that only the brain region was retained, but also reduces the data size and eliminating irrelevant artifacts ensured that the CNN focused only on the region of interest. The cropped brain region was then resized to a uniform dimension of 224×224 pixels and the pixel intensity values were normalized to a $[0,1]$ range to improve numerical stability during feature extraction via convolutional operation of RESNET-50 model. Figure 2 illustrates visual analysis of skull-stripping, and image cropping discussed in the Algorithm 1.

Algorithm 1. Preprocessing operations for brain MRI images

Input: Raw MRI image I

Output: Preprocessed image I_p (224×224)

Start

1. Load MRI image I
2. Convert I to grayscale
3. Apply Gaussian blur to reduce noise
4. Perform thresholding to create binary mask
5. Apply morphological operations and do erode and dilate to remove noise
 - Keep largest connected component as brain mask
6. Skull-stripping: → apply mask to retain only brain region
7. Detect contours of brain mask
 - Find extreme points (top, bottom, left, right)
 - Crop image around brain bounding box
8. Resize cropped image to 224×224 pixels
9. Normalize pixel intensities to $[0,1]$
10. Return preprocessed image I_p

End

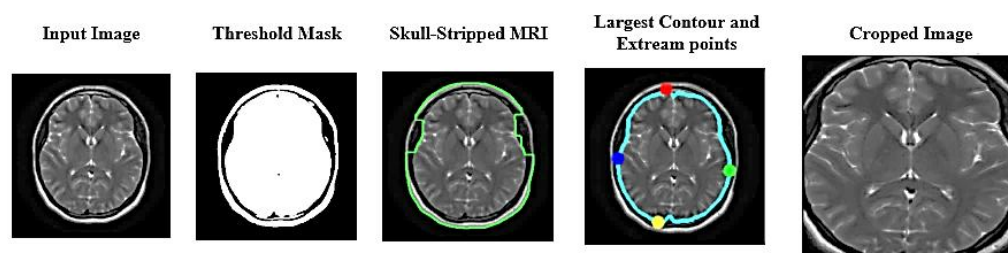


Figure 2. Visualization of the skull stripping and image cropping

2.3. Feature extraction

The study considers feature extraction strategy to learn discriminative representations of brain MRI images via transfer learning using the ResNet-50 CNN architecture. A lightweight FW mechanism is integrated to emphasize features that are relevant for classification. The ResNet-50 model is pretrained on the ImageNet dataset and provides a strong initialization for extracting features, which enables the network to capture both low-level structural details and high-level semantic information, reduces the dependency on manual feature engineering, and improves the speed of model convergence. The model considers batch of

preprocessed images $I_p \in \mathbb{R}^{H \times W \times C}$ subjected to convolutional layers of ResNet-50, which generates a feature map $F = \{f_1, f_2 \dots f_c\} \in \mathbb{R}^{h \times w \times C}$. Here, C is the number of feature channel and each $f_c \in \mathbb{R}^{h \times w}$ that denotes the the spatial feature response of the c -th filter.

The extracted feature maps contain rich information but all features may not contribute to classification tasks as they are often associated with noisy information and redundant responses. To address this, the proposed study implements FW layer, where the obtained feature map F are processed via various transformation operation to compute a weight vector that quantifies the relative contribution of each feature channel. The first operation is the weight initialization to compute activation strength of each channel using following numerical operation:

$$z_c = \frac{h \times w}{\sum_{i=1}^h \sum_{j=1}^w \frac{1}{F_c(i,j) + \epsilon}} \quad (1)$$

where, ϵ is a small constant to avoid division by zero. The above operation basically produce a descriptor vector that aggregates the channels with strong activations i.e., likely tumor regions are favored and it also penalizes low activations. The obtained descriptors are then transformed into FW using a nonlinear mapping operation as (2):

$$\alpha = \sigma(W_2 \delta(W_1 z)), W_1 \in \mathbb{R}^{\frac{C}{r} \times C}, W_2 \in \mathbb{R}^{C \times \frac{C}{r}} \quad (2)$$

where, α represents the FW for all channels, W_1 and W_2 are the projection matrix, r is a reduction ratio to maintain computational efficiency, δ is a linear rectifier that ensures negatives are cut off at zero, and σ denotes sigmoid operation which further ensures $\alpha_c \in (0,1)$. Afterwards each feature channel is scaled according to its weight such that: $\hat{F}_c = \alpha_c \cdot F_c$, which produces a weighted feature tensor $\hat{F}$. This mechanism ensures that highly discriminative tumor features (irregular boundaries, abnormal textures) are emphasized much and irrelevant, and redundant responses are ignored. The enhanced feature map $\hat{F}$ are reduced in dimensionality via GAP and flattened to form a compact one-dimensional vector such that: $v = \text{Flatten}(\text{GAP}(\hat{F})) \in \mathbb{R}^d$, where d is the final feature vector length. This vector serves as the input to the SVM classifier described in the next section.

2.4. Tumor classification and grading

The classification stage of the proposed framework employs a multi-class SVM as the final decision module. Instead of conventional fully connected (FC) layers with SoftMax activation, the extracted feature vector $v \in \mathbb{R}^d$ is fed into an SVM classifier trained using a one-vs-rest (OvR) strategy. The SVM provides robust decision boundaries, which are less prone to overfitting when compared to FC-based classifiers, especially in scenarios involving limited medical imaging data. Therefore, given a set of training feature vectors $\{v_i, y_i\}_{i=1}^N$, where $y_i \in \{1, 2, \dots, K\}$ denotes the class label, the SVM aims to learn multiple hyperplanes as expressed in (3), where w_k and b_k define the separating hyperplane for class k and the predicted class is determined as in (4). Table 2 illustrates the a layer wise details of the model.

$$f_k(v) = w_k^T v + b_k, k = 1, 2, \dots, K \quad (3)$$

$$\hat{y} = \arg \max_k f_v(v) \quad (4)$$

Table 2. Layer details of the proposed hybrid CNN–SVM framework

Stage	Operation	Parameters	Output dimension
Input	MRI image (after preprocessing)	Size=224×224×3	(224, 224, 3)
Batching	Mini-batch processing	Batch size=32 (forward pass-through CNN)	(32, 224, 224, 3)
CNN backbone	ResNet-50 (pretrained on ImageNet, convolutional layers only, frozen weights)	No training; used only for feature extraction	(7, 7, 2048) after final conv block
FW	Channel-wise weighting (lightweight re-scaling mechanism)	Weights vector size=2048 (values $\in [0,1]$)	(7, 7, 2048)
Flattening	Vectorization of pooled features	–	(1, 2048)
SVM classifier	Multi-class SVM with probability estimation	Kernel=RBF, C=0, $\gamma=0.01$, Strategy=OvR, probability=True	3-class (Figshare), 4-class (Kaggle), 2-class (BraTS)
Grading mapping	Clinical label assignment	Glioma→Malignant; Meningioma & Pituitary → Benign; No tumor → Healthy	Malignant/Benign/Healthy

3. RESULTS

The implementation of the proposed system uses a workstation with an Intel Core i7 processor, NVIDIA GPU, Windows operating environment, and 32 GB RAM. All experiments are conducted in Python through the Anaconda distribution with Jupyter Notebook as the development interface. This section presents the outcomes of the proposed hybrid CNN–SVM framework on three publicly available benchmark datasets: Figshare, BraTS-2019, and Kaggle MRI. The performance is measured using accuracy, precision, recall, and F1-score, which are standard metrics in classification tasks. Figures 3–5 show the confusion matrices for the Figshare, BraTS-2019, and Kaggle MRI datasets, respectively which display the class-wise distribution of correctly and incorrectly predicted samples. The detailed numerical results in terms of precision, recall, F1-score, and overall accuracy, are reported in Table 3.

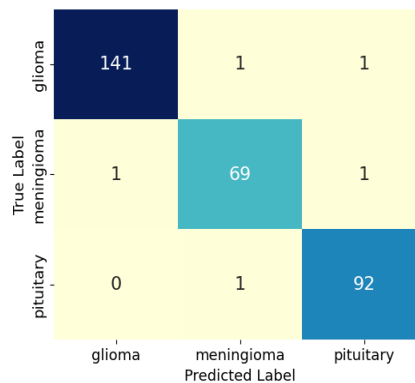


Figure 3. Confusion matrix on Figshare dataset

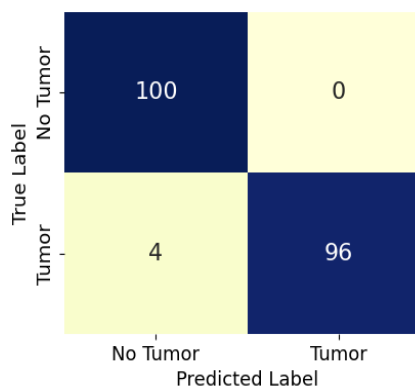


Figure 4. Confusion matrix on BraTS-2019 dataset

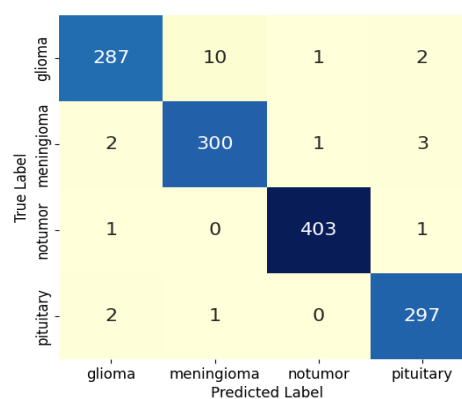


Figure 5. Confusion matrix on Kaggle MRI dataset

Table 3. Presents classification outcome on all the datasets

Dataset	Class	Precision (%)	Sensitivity (%)	Specificity (%)	F1-score (%)	Support
Figshare	Glioma	99	98	99.39	99	143
	Meningioma	96	97	99.15	97	71
	Pituitary tumor	99	99	99.07	99	93
	Overall accuracy	98.6	—	—	—	—
BraTS-2019	No tumor	96.15	100	96.00	98.03	100
	Tumor	100	96	100	97.9	100
	Overall accuracy	98	—	—	—	—
	Overall accuracy	98	—	—	—	—
Kaggle MRI	Glioma	99	96	99	97	300
	Meningioma	96	98	97	97	306
	No tumor	100	100	100	100	405
	Pituitary tumor	98	99	98	99	300
	Overall accuracy	98.17	—	—	—	—

The visual analysis from Figures 3–5 and the quantitative outcomes in Table 3 demonstrate that the proposed CNN–SVM framework achieves consistently high performance across all three benchmark datasets. On the Figshare dataset, the model reached an overall accuracy of 98.6%, with sensitivity above 97% and specificity exceeding 98% for glioma, meningioma, and pituitary tumor classes. On the BraTS-2019 dataset, designed for binary classification, the system attained 98% accuracy, with 100% sensitivity for non-tumor scans and 96% sensitivity for tumor cases, supported by specificity near 98%. On the Kaggle MRI dataset with four classes, the framework delivered 98.17% accuracy, maintaining sensitivity and specificity above 97% for all categories. The outcome highlights effectiveness of the proposed model in terms of precision and F1-score but also its clinical importance in terms of sensitivity (true positive rate) and specificity (true negative rate), both of which are critical for reducing misdiagnosis in neuroimaging tasks.

3.1. Discussion

Table 4 compares the proposed CNN–SVM framework with existing approaches. The prior works such as Khan *et al.* [26] relied on DenseNet feature extraction with conventional machine learning classifiers but their performance (95.10%) was limited by the relatively small dataset size and the sensitivity of handcrafted feature–classifier. Subba and Sunaniya [27] introduced attention-based GoogLeNet, which improved multiscale feature representation but has high model complexity. Similarly, deep CNN in [28] faced overfitting issues when trained on limited datasets, and explainable artificial intelligence (XAI)-enhanced model in [29] achieved interpretability but sacrificed accuracy (95.42%) owing to increased architectural overhead. On the Kaggle MRI dataset, hybrid CNN–LSTM [30], and autoencoder-based CNNs [22] underperformed (92%–93.4%), due to their sensitivity to longer training times and weaker discriminative power on fine tumor boundaries. Even transfer learning with deeper models such as Xception and DenseNet [31] reached only 95.87%.

Table 4. Comparative analysis with recent work in literature

Ref	Dataset	Method	Accuracy (%)
Khan <i>et al.</i> [26]	Figshare	Hybrid-NET model	95.10
Subba and Sunaniya [27]	Figshare	CNN+Softmax	97.62
Vankdothu <i>et al.</i> [30]	Kaggle MRI	CNN, LSTM	92
Saeedi <i>et al.</i> [22]	Kaggle MRI	CNN+autoencoder	93.4
Asif <i>et al.</i> [31]	Kaggle MRI	DL+transfer learning	95.87
Sadr <i>et al.</i> [28]	Figshare	Deep CNN	97.27
Ullah <i>et al.</i> [29]	Figshare	Custom DL+attention	95.42
Proposed	Kaggle MRI	CNN+FW+SVM	98.17
Proposed	Figshare	CNN+FW+SVM	98.6

The reason behind achieving better performance by the proposed system are: i) CNN-based feature extraction enhanced by the proposed FW mechanism, which eliminates redundant channels and emphasizes discriminative regions; ii) the use of SVM as a classifier, which provides more stable decision boundaries than SoftMax, and iii) a preprocessing operation that reduces noise and improves generalization. To further validate the design choices, an ablation study was conducted and the results are presented in Table 5. The ablation study showed that ResNet-50 with a FC classifier achieved 96.2% accuracy, and outperformed other baseline models. But when using SVM instead of SoftMax accuracy improved to 97.3%, and the consideration of the FW module further increased it to 98.17% with a macro-F1 of 98.1%. On the other hand the preprocessing operations such as skull-stripping and cropping also showed significant impact on the model performance, as their removal caused consistent drops in accuracy. The model also showed sensitivity

to training size and the outcome findings confirms that the proposed hybrid design offers a simple and effective alternative to conventional DL models.

Table 5. Ablation study results on Kaggle MRI dataset

Variant	Accuracy (%)	Macro-F1 (%)	Remark
ResNet-50+FC	96.2	95.8	Best among standard CNN backbones
VGG16+FC	94.7	94.2	Lower accuracy due to heavier params, less efficient features
MobileNet+FC	95.3	94.9	Lightweight but weaker on fine tumor distinctions
ResNet-50+SVM	97.3	96.9	SVM improves decision boundaries over SoftMax
ResNet-50+FW+ FC	98	97.7	Improved result but reduced recall on Glioma
Proposed (ResNet-50+FW+SVM)	98.17	98.1	Best overall
Proposed (linear SVM kernel)	97.5	97.2	Slightly lower, less flexible boundary
Proposed (RBF kernel, default)	98.17	98.1	Optimal balance
Proposed w/o skull-stripping	97.6	97.3	Background noise hurts performance
Proposed w/o cropping	97.9	97.5	Retains more non-brain tissue
Proposed full (skull-strip+crop)	98.17	98.1	Best preprocessing pipeline
Proposed (train 80%, test 20)	98.17	98.1	Main experimental setup
Proposed (train 70%, test 30)	97.6	97.3	Accuracy drops due to fewer training samples
Proposed (train 40%, test 60)	96.8	96.2	Significant decline due to limited training

Moreover, most publicly available neuroimaging datasets lack histopathological grading labels. To address this limitation, this study introduces a clinically inspired grading scheme as illustrated in Figure 6. The framework not only predicts tumor classes with high confidence (94.6%–98.9%) but also maps outputs to clinically meaningful grades. Gliomas are labeled Malignant due to their infiltrative and progressive nature [32]; meningiomas and pituitary tumors are mapped as Benign, aligning with WHO Grade I and adenoma profiles [33], [34]; and non-tumor scans are considered Healthy, crucial for patient triaging. This grading scheme transforms raw predictions into actionable clinical insights.

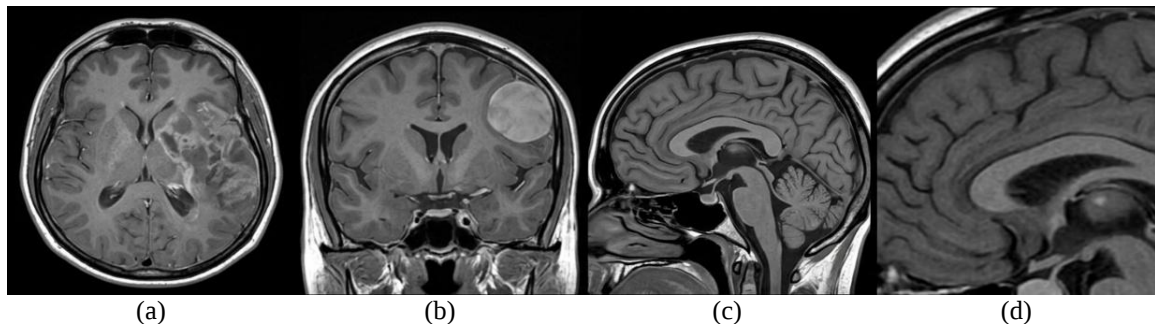


Figure 6. Visual analysis of predicted image along with tumor grad viz; (a) predicted: glioma, grade: malignant, (b) predicted: meningioma, grade: benign, (c) predicted: no tumor, grade: healthy, and (d) predicted: pituitary, grade: benign

3.2. Limitation and clinical consideration

It is to be noted that selected dataset of BraTS-2019, Kaggle MRI, Figshare encapsulates majority of the frequently reported brain tumor viz. pituitary tumors, meningiomas, and gliomas. However, the study doesn't involve other forms like schwannomas and medulloblastomas which is mainly due to their restricted availability as publicly open access dataset repository. However, this exclusion could only limit the generalizability to a very rare forms of tumors. Hence, future direction work can be carried out to consider additional dataset for inclusion of more broader range of tumor subtypes.

The grading process is clinically inspired but not validated against histopathological labels, and other limitation is the centralized nature of the predictive model whereas in real-world hospitals often cannot share patient MRI data due to strict privacy regulations and ethical concerns. In terms of deployment, the proposed framework is envisioned as a decision-support tool rather than a replacement for radiologists. Its integration into clinical workflows can help improve hospital operations, optimize reporting, and resource allocation. However, this study employed publicly available datasets, real-world deployment will require compliance with institutional review protocols and international data protection standards to ensure the secure handling of sensitive patient information. Further, it is to be noted that there is a dependency of

substantial computational resources by hybrid CNN-SVM (e.g., extended training duration, high memory, and dedicated GPU). All such inclusion could easily saturate the performance of resource-constraint ecosystem. Moreover, there is a class imbalance associated with the dataset while a restricted diversity is noted towards image modalities. All these can easily induce bias to influence the performance of model when exposed to heterogeneous clinical samples.

4. CONCLUSION

The proposed study has discussed about a novel neuroimaging analysis for facilitating identification and grading of brain tumor by hybridizing CNN and SVM. The proposed study model improves upon the accuracy of classification, boosting the generalization over different dataset, and retain minimal computational burden which is quite applicable for practical scenario of clinical settings. The feature extraction process is decoupled from classification for facilitating acquisition of complex characteristic of tumor towards ensuring the boundaries of robust decision. When compared with multiple benchmarked datasets, the proposed model exhibited 98.5% of average accuracy of classification with 97% of F1-score and 51.7 ms per image as a response time which is basically a time to generate rapid inference. Cumulatively, the proposed model facilitates effective solution for brain tumor diagnosis with increasing scope of applicability to real-world clinical settings. The future direction of work will be towards combining the explainability methods such as Grad-Cam with an inclusion of three-dimensional volumetric analysis of additional types of tumors for enhanced clinical relevance and acceptance.

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AUTHOR CONTRIBUTIONS STATEMENT

This journal uses the Contributor Roles Taxonomy (CRediT) to recognize individual author contributions, reduce authorship disputes, and facilitate collaboration.

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C : **C**onceptualization

M : **M**ethodology

So : **S**oftware

Va : **V**alidation

Fo : **F**ormal analysis

I : **I**nterpretation

R : **R**esources

D : **D**ata Curation

O : **O**riginal Draft

E : **E**diting

Vi : **V**isualization

Su : **S**upervision

P : **P**roject administration

Fu : **F**unding acquisition

CONFLICT OF INTEREST STATEMENT

Authors state no conflict of interest.

DATA AVAILABILITY

The data that support the findings of this study are available from the corresponding authors, upon reasonable request.

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